SEQUENCE LISTING

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Yoshiki TANI
Satoshi YONEHARA

<120> FRUCTOSYLAMINE OXIDASE

<130> 0020-5361PUS1

<140> US 10/528,992
<141> 2005-03-24

<150> PCT/JP03/11766
<151> 2003-09-16

<150> JP 2002-277214
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<170> PatentIn version 3.1

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aaaccataaa taaatcaaaa ctttcaacaa cggatctctt ggttctggca tcgatgaaga 180

acgcagcaaa atgcgataag taatgtgaat tgcagaattc agtgaatcat cgaatctttg 240

aacgcacatt gcgcccgcca gtattctggc gggcatgcct gttcgagcgt catttcaacc 300

ctcaagcccc cgggtttggt gttggggatc ggcgagccct tgcggcaagc cggccccgaa 360

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1               5                   10                  15

ggg ctc ggt acc gcc tgg gct ttg gcc aaa cga tca cac ttt tcc aac       96
Gly Leu Gly Thr Ala Trp Ala Leu Ala Lys Arg Ser His Phe Ser Asn
            20                  25                  30

acc tcg att act gtc gtc gac gac tgc gca gga cag ttt cct cca gaa      144
Thr Ser Ile Thr Val Val Asp Asp Cys Ala Gly Gln Phe Pro Pro Glu
        35                  40                  45

gat gct gcc agt gta gac tcg tct cgc att gta cga gcc gac tac tcg      192
Asp Ala Ala Ser Val Asp Ser Ser Arg Ile Val Arg Ala Asp Tyr Ser
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gac cct tac tat gcc gcg ctt gcc gcc gag gcg cag aag gaa tgg cga      240
Asp Pro Tyr Tyr Ala Ala Leu Ala Ala Glu Ala Gln Lys Glu Trp Arg
65                  70                  75                  80

aag cag ggt gat cat gag gtc ggt ggg cag gga cga tat tcc gag tcg      288
Lys Gln Gly Asp His Glu Val Gly Gly Gln Gly Arg Tyr Ser Glu Ser
                85                  90                  95

ggc ttt gtt ctc tgc gcg agc gag act cct gaa gac ttc aag ctc aag      336
Gly Phe Val Leu Cys Ala Ser Glu Thr Pro Glu Asp Phe Lys Leu Lys
            100                 105                 110

aag tct ggc atg gac tac acc aag gag agc gcc aaa aac gtc gag ttg      384
Lys Ser Gly Met Asp Tyr Thr Lys Glu Ser Ala Lys Asn Val Glu Leu
        115                 120                 125

att gct aag gag act ggt ctg ccc gtg gat aag atc cag aag ctg gag      432
Ile Ala Lys Glu Thr Gly Leu Pro Val Asp Lys Ile Gln Lys Leu Glu
    130                 135                 140

agt acc aag gct ctc caa gag ttc ctt ggc aca gac ggt tat ccc gga      480
Ser Thr Lys Ala Leu Gln Glu Phe Leu Gly Thr Asp Gly Tyr Pro Gly
145                 150                 155                 160

gac tgg ggc tac ctc aat ggc aac tct ggc tgg gct gat gcc ggg gag      528
Asp Trp Gly Tyr Leu Asn Gly Asn Ser Gly Trp Ala Asp Ala Gly Glu
                165                 170                 175

ggt atg aag tgg ctc tat aag cag gcc cag gcc aca gga cgt att cat      576
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Gly Met Lys Trp Leu Tyr Lys Gln Ala Gln Ala Thr Gly Arg Ile His
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ttt gtc aac ggc aag gtg aca gag ctc gta aca gag ggt gac cga gtc      624
Phe Val Asn Gly Lys Val Thr Glu Leu Val Thr Glu Gly Asp Arg Val
        195                 200                 205

att ggt gcg aaa ttg agc gat tca aag att ctc aag gcc gat gtg gtt      672
Ile Gly Ala Lys Leu Ser Asp Ser Lys Ile Leu Lys Ala Asp Val Val
    210                 215                 220

atg gta gct gct ggt gct tgg tcc ggc tca ctc gtt gac ctt cga gga      720
Met Val Ala Ala Gly Ala Trp Ser Gly Ser Leu Val Asp Leu Arg Gly
225                 230                 235                 240

aga aca gag gct act ggc cat gct gtc gcg tat atg gac atc aca ccg      768
Arg Thr Glu Ala Thr Gly His Ala Val Ala Tyr Met Asp Ile Thr Pro
                245                 250                 255

gaa gag cag aag cga ctc gac aac ttc cct gtg gtg ttg aat ctc agc      816
Glu Glu Gln Lys Arg Leu Asp Asn Phe Pro Val Val Leu Asn Leu Ser
            260                 265                 270

acc ggt ctc ttc ctc att cct cct cga aat aac gtc ctc aag gcc gcc      864
Thr Gly Leu Phe Leu Ile Pro Pro Arg Asn Asn Val Leu Lys Ala Ala
        275                 280                 285

cga cac aca ttc ggg tac att aac ccg gtc aag att aac aac gct ctt      912
Arg His Thr Phe Gly Tyr Ile Asn Pro Val Lys Ile Asn Asn Ala Leu
    290                 295                 300

cct cct tcg ccc aac gat aag cgg gaa cca ttc atc gca tct caa ccc      960
Pro Pro Ser Pro Asn Asp Lys Arg Glu Pro Phe Ile Ala Ser Gln Pro
305                 310                 315                 320

tac acc tct cgc aac gat tcc tca aat cct tta acc gtc gag gct gac     1008
Tyr Thr Ser Arg Asn Asp Ser Ser Asn Pro Leu Thr Val Glu Ala Asp
                325                 330                 335

aaa gat ctg cgc cgc gca ctc acg gat ctg tgt cct ata cgt ggc cta     1056
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            340                 345                 350

gaa acc agg cca tgg aag gag gct cga atc tgc tgg tat tcc gat aca     1104
Glu Thr Arg Pro Trp Lys Glu Ala Arg Ile Cys Trp Tyr Ser Asp Thr
        355                 360                 365

cga gat ggc gag tgg ctc att gac tac cac ccg ggc tgg aag gga ctc     1152
Arg Asp Gly Glu Trp Leu Ile Asp Tyr His Pro Gly Trp Lys Gly Leu
    370                 375                 380

ttt gtt gca aca ggt gac agt gga cac gga ttc aag ttc cta ccc aac     1200
Phe Val Ala Thr Gly Asp Ser Gly His Gly Phe Lys Phe Leu Pro Asn
385                 390                 395                 400

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                405                 410                 415

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ggt gga cgg ccc ttg gtg ctc tgt gat gag ctc gag aag ggc agg gcg     1392
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Thr Ser Ile Thr Val Val Asp Asp Cys Ala Gly Gln Phe Pro Pro Glu
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Asp Ala Ala Ser Val Asp Ser Ser Arg Ile Val Arg Ala Asp Tyr Ser
    50                  55                  60

Asp Pro Tyr Tyr Ala Ala Leu Ala Ala Glu Ala Gln Lys Glu Trp Arg
65                  70                  75                  80

Lys Gln Gly Asp His Glu Val Gly Gly Gln Gly Arg Tyr Ser Glu Ser
                85                  90                  95

Gly Phe Val Leu Cys Ala Ser Glu Thr Pro Glu Asp Phe Lys Leu Lys
            100                 105                 110

Lys Ser Gly Met Asp Tyr Thr Lys Glu Ser Ala Lys Asn Val Glu Leu
        115                 120                 125

Ile Ala Lys Glu Thr Gly Leu Pro Val Asp Lys Ile Gln Lys Leu Glu
    130                 135                 140

Ser Thr Lys Ala Leu Gln Glu Phe Leu Gly Thr Asp Gly Tyr Pro Gly
145                 150                 155                 160
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Asp Trp Gly Tyr Leu Asn Gly Asn Ser Gly Trp Ala Asp Ala Gly Glu
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Gly Met Lys Trp Leu Tyr Lys Gln Ala Gln Ala Thr Gly Arg Ile His
            180                 185                 190

Phe Val Asn Gly Lys Val Thr Glu Leu Val Thr Glu Gly Asp Arg Val
        195                 200                 205

Ile Gly Ala Lys Leu Ser Asp Ser Lys Ile Leu Lys Ala Asp Val Val
    210                 215                 220

Met Val Ala Ala Gly Ala Trp Ser Gly Ser Leu Val Asp Leu Arg Gly
225                 230                 235                 240

Arg Thr Glu Ala Thr Gly His Ala Val Ala Tyr Met Asp Ile Thr Pro
                245                 250                 255

Glu Glu Gln Lys Arg Leu Asp Asn Phe Pro Val Val Leu Asn Leu Ser
            260                 265                 270

Thr Gly Leu Phe Leu Ile Pro Pro Arg Asn Asn Val Leu Lys Ala Ala
        275                 280                 285

Arg His Thr Phe Gly Tyr Ile Asn Pro Val Lys Ile Asn Asn Ala Leu
    290                 295                 300

Pro Pro Ser Pro Asn Asp Lys Arg Glu Pro Phe Ile Ala Ser Gln Pro
305                 310                 315                 320

Tyr Thr Ser Arg Asn Asp Ser Ser Asn Pro Leu Thr Val Glu Ala Asp
                325                 330                 335

Lys Asp Leu Arg Arg Ala Leu Thr Asp Leu Cys Pro Ile Arg Gly Leu
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Glu Thr Arg Pro Trp Lys Glu Ala Arg Ile Cys Trp Tyr Ser Asp Thr
        355                 360                 365

Arg Asp Gly Glu Trp Leu Ile Asp Tyr His Pro Gly Trp Lys Gly Leu
    370                 375                 380

Phe Val Ala Thr Gly Asp Ser Gly His Gly Phe Lys Phe Leu Pro Asn
385                 390                 395                 400

Leu Gly Glu Lys Ile Val Asp Val Met Gln Gly Gln Gly Gly Lys Leu
                405                 410                 415

Gly Glu Lys Trp Arg Trp Lys Glu Ile Gln Asn Asp Gly Val Gly Arg
            420                 425                 430

Glu Thr Asn Gly Val Tyr Thr Gly Leu Val Thr Glu Asp Gly Ser Arg
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Gly Gly Arg Pro Leu Val Leu Cys Asp Glu Leu Glu Lys Gly Arg Ala
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gtt ggt ggc gga act tgg gga tgc tca act gcc ctc cat ctc gcc cgt       96
Val Gly Gly Gly Thr Trp Gly Cys Ser Thr Ala Leu His Leu Ala Arg
            20                  25                  30

cgg ggt tac acc aac gtc act gtt ctc gat gtc aat cgc atc ccg tca      144
Arg Gly Tyr Thr Asn Val Thr Val Leu Asp Val Asn Arg Ile Pro Ser
        35                  40                  45

ccg ata tca gcc ggg cat gat gta aac aaa ctt tct aac aga cta ggc      192
Pro Ile Ser Ala Gly His Asp Val Asn Lys Leu Ser Asn Arg Leu Gly
    50                  55                  60

act tct gat agt aaa ggc gat gac gaa gac tca atc tgg aaa gct ctt      240
Thr Ser Asp Ser Lys Gly Asp Asp Glu Asp Ser Ile Trp Lys Ala Leu
65                  70                  75                  80

acg tac gcc gca gct caa gga tgg ctc cat gat ccc atc ttc caa cct      288
Thr Tyr Ala Ala Ala Gln Gly Trp Leu His Asp Pro Ile Phe Gln Pro
                85                  90                  95

ttc tgc cac aat aca gga gct gtc atg gct ggc tca aca cca aaa tct      336
Phe Cys His Asn Thr Gly Ala Val Met Ala Gly Ser Thr Pro Lys Ser
            100                 105                 110

atc aag cag ctg gta gaa gat gag atc ggt gac gac atc gac cag tat      384
Ile Lys Gln Leu Val Glu Asp Glu Ile Gly Asp Asp Ile Asp Gln Tyr
        115                 120                 125

aca cct ctc aac aca gca gaa gat ttc aga agg act atg ccg gag cgt      432
Thr Pro Leu Asn Thr Ala Glu Asp Phe Arg Arg Thr Met Pro Glu Arg
    130                 135                 140

att ctg aca ggt gat ttt cta ggc tgg aag ggc ttt tac aag ccc aga      480
Ile Leu Thr Gly Asp Phe Leu Gly Trp Lys Gly Phe Tyr Lys Pro Arg
145                 150                 155                 160

ggt tca ggt tgg gtt cat gcc aga aag gct atg aaa gct gct ttt gaa      528
Gly Ser Gly Trp Val His Ala Arg Lys Ala Met Lys Ala Ala Phe Glu
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                 165                 170                 175

gag agc cag aga ctt ggt gtc aag ttc atc act ggc tct ccc gaa ggc      576
Glu Ser Gln Arg Leu Gly Val Lys Phe Ile Thr Gly Ser Pro Glu Gly
             180                 185                 190

aag gtc gag agt ctg gtc ttt gaa gct ggt gat gtc aaa ggt gca aaa      624
Lys Val Glu Ser Leu Val Phe Glu Ala Gly Asp Val Lys Gly Ala Lys
         195                 200                 205

aca gca gat gga aag gaa cac aga gcg gat cga aca att ctc tcc gct      672
Thr Ala Asp Gly Lys Glu His Arg Ala Asp Arg Thr Ile Leu Ser Ala
     210                 215                 220

ggt gcc tca gca gag ttc tcc ctc gat ttt gag aac cag atc cgt cct      720
Gly Ala Ser Ala Glu Phe Ser Leu Asp Phe Glu Asn Gln Ile Arg Pro
225                 230                 235                 240

acg gca tgg act ctg ggc cat atc cag atg aca gca gag gaa aca aag      768
Thr Ala Trp Thr Leu Gly His Ile Gln Met Thr Ala Glu Glu Thr Lys
                245                 250                 255

ctg tac aag gaa ctt ccc ccc ctt ttc aat atc aac cag ggc ttc ttc      816
Leu Tyr Lys Glu Leu Pro Pro Leu Phe Asn Ile Asn Gln Gly Phe Phe
             260                 265                 270

atg gaa ccc gat gag gac ttg cat caa ctc aag atg tgc gat gaa cat      864
Met Glu Pro Asp Glu Asp Leu His Gln Leu Lys Met Cys Asp Glu His
         275                 280                 285

ccc gga tac tgc aat tgg gtt gac aaa cct ggt tcc aaa tac ccc cag      912
Pro Gly Tyr Cys Asn Trp Val Asp Lys Pro Gly Ser Lys Tyr Pro Gln
     290                 295                 300

tcc atc ccc ttc gca aag tat caa gtg cca att gag gct gaa cga cgc      960
Ser Ile Pro Phe Ala Lys Tyr Gln Val Pro Ile Glu Ala Glu Arg Arg
305                 310                 315                 320

atg aag caa ttt ctg aaa gac atc atg cct cag ctc gca gat cgg cca     1008
Met Lys Gln Phe Leu Lys Asp Ile Met Pro Gln Leu Ala Asp Arg Pro
                325                 330                 335

ctt gtt cat gct cga atc tgc tgg tgc gcc gat aca cag gat aga atg     1056
Leu Val His Ala Arg Ile Cys Trp Cys Ala Asp Thr Gln Asp Arg Met
             340                 345                 350

ttt ctg atc acg tat cac cct cga cac cca tcg ctt gtc att gct tcc     1104
Phe Leu Ile Thr Tyr His Pro Arg His Pro Ser Leu Val Ile Ala Ser
         355                 360                 365

ggg gat tgt ggc aca gga tac aag cat atc act tcc att gga aag ttc     1152
Gly Asp Cys Gly Thr Gly Tyr Lys His Ile Thr Ser Ile Gly Lys Phe
     370                 375                 380

atc tct gat tgt atg gag ggc aca ttg gag gaa agg ttt gct aag ttc     1200
Ile Ser Asp Cys Met Glu Gly Thr Leu Glu Glu Arg Phe Ala Lys Phe
385                 390                 395                 400
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tgg aga tgg cga cca gag aag ttt acg gag ttc tgg ggt aaa gat ccc     1248
Trp Arg Trp Arg Pro Glu Lys Phe Thr Glu Phe Trp Gly Lys Asp Pro
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ctg gat cgg ttt gga gct gac gat aag atc atg gat ttg ccc aag agt     1296
Leu Asp Arg Phe Gly Ala Asp Asp Lys Ile Met Asp Leu Pro Lys Ser
            420                 425                 430

gat gca gag gga tgg aca gac ata cag aat gat aaa taa                 1335
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Arg Gly Tyr Thr Asn Val Thr Val Leu Asp Val Asn Arg Ile Pro Ser
        35                  40                  45

Pro Ile Ser Ala Gly His Asp Val Asn Lys Leu Ser Asn Arg Leu Gly
    50                  55                  60

Thr Ser Asp Ser Lys Gly Asp Asp Glu Asp Ser Ile Trp Lys Ala Leu
65                  70                  75                  80

Thr Tyr Ala Ala Ala Gln Gly Trp Leu His Asp Pro Ile Phe Gln Pro
                85                  90                  95

Phe Cys His Asn Thr Gly Ala Val Met Ala Gly Ser Thr Pro Lys Ser
            100                 105                 110

Ile Lys Gln Leu Val Glu Asp Glu Ile Gly Asp Asp Ile Asp Gln Tyr
        115                 120                 125

Thr Pro Leu Asn Thr Ala Glu Asp Phe Arg Arg Thr Met Pro Glu Arg
    130                 135                 140

Ile Leu Thr Gly Asp Phe Leu Gly Trp Lys Gly Phe Tyr Lys Pro Arg
145                 150                 155                 160

Gly Ser Gly Trp Val His Ala Arg Lys Ala Met Lys Ala Ala Phe Glu
                165                 170                 175

Glu Ser Gln Arg Leu Gly Val Lys Phe Ile Thr Gly Ser Pro Glu Gly
            180                 185                 190

Lys Val Glu Ser Leu Val Phe Glu Ala Gly Asp Val Lys Gly Ala Lys
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        195                 200                 205

Thr Ala Asp Gly Lys Glu His Arg Ala Asp Arg Thr Ile Leu Ser Ala
    210                 215                 220

Gly Ala Ser Ala Glu Phe Ser Leu Asp Phe Glu Asn Gln Ile Arg Pro
225                 230                 235                 240

Thr Ala Trp Thr Leu Gly His Ile Gln Met Thr Ala Glu Glu Thr Lys
                245                 250                 255

Leu Tyr Lys Glu Leu Pro Pro Leu Phe Asn Ile Asn Gln Gly Phe Phe
            260                 265                 270

Met Glu Pro Asp Glu Asp Leu His Gln Leu Lys Met Cys Asp Glu His
        275                 280                 285

Pro Gly Tyr Cys Asn Trp Val Asp Lys Pro Gly Ser Lys Tyr Pro Gln
    290                 295                 300

Ser Ile Pro Phe Ala Lys Tyr Gln Val Pro Ile Glu Ala Glu Arg Arg
305                 310                 315                 320

Met Lys Gln Phe Leu Lys Asp Ile Met Pro Gln Leu Ala Asp Arg Pro
                325                 330                 335

Leu Val His Ala Arg Ile Cys Trp Cys Ala Asp Thr Gln Asp Arg Met
            340                 345                 350

Phe Leu Ile Thr Tyr His Pro Arg His Pro Ser Leu Val Ile Ala Ser
        355                 360                 365

Gly Asp Cys Gly Thr Gly Tyr Lys His Ile Thr Ser Ile Gly Lys Phe
    370                 375                 380

Ile Ser Asp Cys Met Glu Gly Thr Leu Glu Glu Arg Phe Ala Lys Phe
385                 390                 395                 400

Trp Arg Trp Arg Pro Glu Lys Phe Thr Glu Phe Trp Gly Lys Asp Pro
                405                 410                 415

Leu Asp Arg Phe Gly Ala Asp Asp Lys Ile Met Asp Leu Pro Lys Ser
            420                 425                 430

Asp Ala Glu Gly Trp Thr Asp Ile Gln Asn Asp Lys
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Cys Asn Arg Ala Tyr Gly Ala
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<210> 8
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<213> Artificial Sequence

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sarium proliferatum

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1 5 10 15

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